DIVERSITY OF MIDSTREAM URINARY BACTERIA IN CHRONIC KIDNEY DISEASE PATIENTS: A PRELIMINARY CULTURE-BASED STUDY

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Introduction: Chronic kidney disease (CKD) is a global disease. Diabetes and hypertension are major risk factors for CKD, while bacterial colonization in the urinary system causes rapid disease progression. **Objectives:** To identify the urinary bacterial diversity in diabetic and hypertensive nephropathy patients rather than identifying urinary infections and study the alteration in bacterial diversity with CKD progression. **Methods:** Mid-stream clean catch urine samples were collected from the study subjects (*n*=105), including diabetic nephropathy (DN), hypertensive nephropathy (HT), CKD with both diabetes and hypertension (HD), other aetiology of CKD (O), and healthy controls (HC). Urine samples were cultured using cystine lactose electrolyte-deficient agar medium, and a panel of biochemical tests was used to identify the bacterial species. **Results:** Bacterial growth was observed in only 31.43% of urine samples. *Escherichia coli*, *Klebsiella* spp., and *Staphylococcus aureus* were predominantly identified in DN patients with the highest mean bacterial load (DN: $>10^5$ CFU mL^{-1}, HT, HD, and O: between 10^4 and10^5 CFU mL^{-1} and HC: $<10^4$ CFU mL^{-1}). *Pseudomonas* spp. was the most predominant bacteria isolated from HT, HD, and O CKD study groups. Further, *Escherichia coli* and *Klebsiella* spp. had been predominantly isolated from early-stage (stages 1-3) CKD patients. In contrast, *Pseudomonas* spp. and *Enterobacter* spp. had been isolated from late-stage (stages 4-5) CKD patients. **Conclusions:** The findings suggest that diabetes predisposes to urinary bacterial colonization in CKD, while greater bacterial diversity is associated with increased disease progression. Further validation is required with a large cohort before clinical application.

Keywords: Chronic kidney disease, Diabetes, Hypertension, and Urinary bacteria

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Abstract

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Introduction

The global burden of chronic kidney disease (CKD) is increasing substantially, with a high mortality rate. Apart from the common causes of CKD, diabetes and hypertension, colonization of both pathogenic and non-pathogenic bacteria in the urinary tract and bladder is another crucial cause of CKD and its progression (Khasriya et al., 2013).

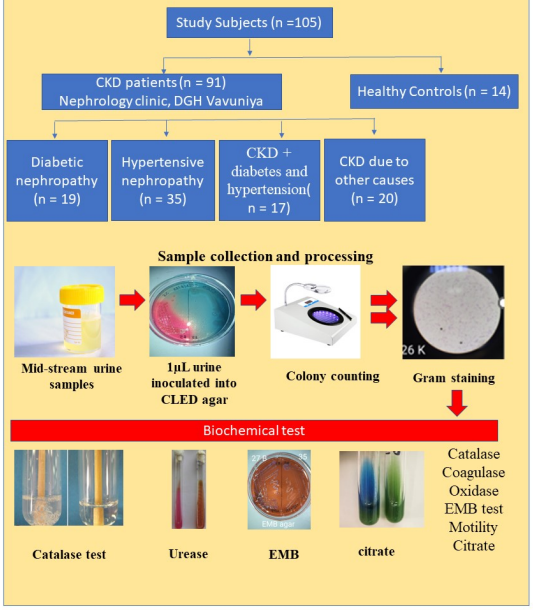
Impaired host defense facilitates the growth and colonization of bacteria in the urine of CKD. Severe reduction of the estimated glomerular filtration rate (eGFR) in CKD prevents the flushing action of urine and eventually causes bacterial colonization (Bien et al., 2012). The presence of glycosuria favors bacterial growth inside the bladder. In addition, the bacterial communities in the urine of patients with renal disease trigger immune responses and cause further damage to the kidney (Geerlings et al., 2014).

Objective

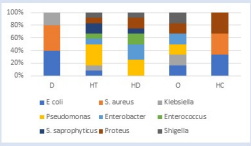
To identify the diversity of urinary bacteria in diabetic and hypertensive CKD patients in comparison with healthy controls using culture-based techniques.

Methodology

Ethical approval was obtained from the ethics review committee of PGIS, University of Peradeniya.



Results



Relative abundance of urinary bacteria in CKD with different causes.

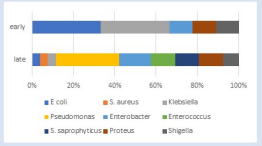


Figure 2: Relative abundance of urinary bacteria in CKD based on the CKD stage

Discussion

The diversity of bacteria had increased in CKD patients with diabetes and hypertension. However, the presence of glycosuria would increase the colonization of bacteria in urine by providing nutritional supplementation for the growth of bacteria (Geerlings et al., 2014). Further, bacterial diversity had been increased in late-stage CKD than in the early stage. This finding suggests that the decrease in urine excretion prevents the innate immune mechanism of the body from flushing the bacteria present in urine and eventually causes bacterial colonization. Kramer et al., (2018) proved Corynebacterium and Staphylococcus spp. were the predominant bacterial spp. identified in CKD urine using metagenomic analysis. However present culture-based study isolated Escherichia coli as the dominant bacterium among CKD patients irrespective, of the aetiology of CKD.

Conclusion

Diabetic nephropathy facilitates bacterial colonization in urine more than other causes of CKD. The diversity of urine bacteria is increased with disease progression. This uncovering the bacterial diversity in CKD groups and stages may inform microbiome-targeted therapies for urine infections among CKD patients.

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